\_\_\_\_\_\_

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: Tue Sep 04 14:58:00 EDT 2007

\_\_\_\_\_

## Validated By CRFValidator v 1.0.3

Application No: 10573658 Version No: 1.0

Input Set:

Output Set:

**Started:** 2007-08-20 10:49:56.980

**Finished:** 2007-08-20 10:49:59.210

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 230 ms

Total Warnings: 59

Total Errors: 32

No. of SeqIDs Defined: 59

Actual SeqID Count: 59

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W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(3)
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W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(8)
W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(9)
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W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(13)
W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(14)
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W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial o	r	Unknown	found	in	<213>	in	SEQ	ID	(20)

### Input Set:

## Output Set:

**Started:** 2007-08-20 10:49:56.980 **Finished:** 2007-08-20 10:49:59.210

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 230 ms

Total Warnings: 59

Total Errors: 32

No. of SeqIDs Defined: 59

Actual SeqID Count: 59

# Error code Error Description

		This error has occured more than 20 times, will not be displayed
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
T.		
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
Ε	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed

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      LASKO, DANA
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<130> 1912-0330PUS1
<140> 10573658
<141> 2007-08-20
<150> PCT/CA04/01763
<151> 2004-09-29
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<220>

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Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
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gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192 Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 55 60

aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca 240
Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser
65 70 75 80

aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg 288
Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat 336
Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr
100 105 110

tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att

184

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile

115

120

125

aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat 432 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140

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Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

ttt gca gga aga cca att att aca caa ttt aaa gta gca aaa ggc tca 528 Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 175

aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa 576 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

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atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu	624
195 200 205	
tct tct gat ggt aaa caa ata ata ata aca gca aca atg atg ggc aca	672
Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 210 215 220	
gct atc aat cct aaa gaa ttc gtg atg gaa tcc cgc aaa cgc gca agg	720
Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg	
225 230 235 240	
cag aca tac acc cgg tac cag act cta gag cta gag aag gag ttt cac	768
Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His	
245 250 255	
tte aat ege tae ttg ace egt egg ega agg ate gag ate gee eae gee	816
Phe Asn Arg Tyr Leu Thr Arg Arg Arg Ile Glu Ile Ala His Ala	
260 265 270	
	964
ctg tgc ctc acg gag cgc cag ata aag att tgg ttc cag aat cgg cgc Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg	864
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Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 55 60

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

45

40

35

Asn Gly	, Lys L	eu Arg	Gln 2	Asn	Lys	Gly	Val	Ile 75	Asn	Gly	Phe	Pro	Ser 80
Asn Lei	ı Ile L	ys Gln 85	Val (	Glu	Leu	Leu	Asp 90	Lys	Ser	Phe	Asn	Lys 95	Met
Lys Thi		lu Asn	Ile 1	Met	Leu	Phe 105	Arg	Gly	Asp	Asp	Pro 110	Ala	Tyr
Leu Gly	7 Thr G	lu Phe	Gln 2	Asn	Thr 120	Leu	Leu	Asn	Ser	Asn 125	Gly	Thr	Ile
Asn Lys		la Phe		Lys 135	Ala	Lys	Ala	Lys	Phe 140	Leu	Asn	Lys	Asp
Arg Let	ı Glu T	yr Gly	Tyr :	Ile	Ser	Thr	Ser	Leu 155	Met	Asn	Val	Ser	Gln 160
Phe Ala	a Gly A	rg Pro. 165	Ile :	Ile	Thr	Gln	Phe 170	Lys	Val	Ala	Lys	Gly 175	Ser
Lys Ala	_	yr Ile 80	Asp I	Pro	Ile	Ser 185	Ala	Phe	Gln	Gly	Gln 190	Leu	Glu
Met Le	Leu P 195	ro Arg	His :		Thr 200	Tyr	His	Ile	Asp	Asp 205	Met	Arg	Leu
Ser Ser 210	_	ly Lys		Ile 215	Ile	Ile	Thr	Ala	Thr 220	Met	Met	Gly	Thr
Ala Ile 225	e Asn P	ro Lys	Glu I 230	Phe	Val	Met	Glu	Ser 235	Arg	Lys	Arg	Ala	Arg 240
Gln Thi	Tyr T	hr Arg 245	Tyr (	Gln	Thr	Leu	Glu 250	Leu	Glu	Lys	Glu	Phe 255	His
Phe Asr	_	yr Leu 60	Thr A	Arg	Arg	Arg 265	Arg	Ile	Glu	Ile	Ala 270	His	Ala
Leu Cy:	Leu T 275	hr Glu	Arg (	Gln	Ile 280	Lys	Ile	Trp	Phe	Gln 285	Asn	Arg	Arg

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	_	stri								_					
	(010	DCII.	a L am	DOC.	A	AIII / C	<i>a</i> 110 2	111001	шар	Jara	DCq.	acric	- •		
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Gly Se	r ser	AIG		Asp	ьeu	GIII	Ald	_	ASII	АІА	тут	ser		ASII	
1			5					10					15		
															0.6
caa aa							_						-		96
Gln Ly:	s Ala	_	Ser	Asn	Thr	Tyr		GLu	Phe	Thr	Asn		Asp	GIn	
		20					25					30			
gca aa	_				-	_			_				_		144
Ala Ly:		Trp	Gly	Asn	Ala		Tyr	Lys	Lys	Tyr	_	Leu	Ser	Lys	
	35					40					45				
tca ga	a aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
Ser Gl	u Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
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Asn Gl	y Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65				70					75					80	
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Asn Le	u Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
			85					90					95		
aag ac	c cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	336
Lys Th	r Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
		100					105					110			
tta gg	a aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	384
Leu Gl	y Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	
	115					120					125				
aat aa	a acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Asn Ly	s Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	
13	0				135					140					
aga ct	t gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtc	tct	caa	480
Ara Lei	=					_				_		_			

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145 150 155 160

ttt gca gga aga cca att att aca caa ttt aaa gta gca aaa ggc tca 528 Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 576 aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 185 624 atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 tct tct gat ggt aaa caa ata att aca gca aca atg atg ggc aca 672 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 210 215 220 gct atc aat cct aaa gaa ttc cgc cag atc aag att tgg ttc cag aat 720 Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn 225 230 235 768 cgt cgc atg aag tgg aag aag gtc gac tcg agc ggc cgc atc gtg act Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr 245 250 774 gac tga

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Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys 35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 55 60 Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 65 70 Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 85 90 95 Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 100 105 110 Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 115 120 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 145 150 155 160 Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 170 175 165 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190 Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205 Ser Ser Asp Gly Lys Gln Ile Ile Ihr Ala Thr Met Met Gly Thr 210 215 220 Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn 225 230 235 240

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288

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caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa	96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln	50
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35 40 45	
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Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile	
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65 70 75 80	

aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met